

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Kathleen L. Horwath et al.

Examiner:

Serial No.: (not yet assigned)

Group No.:

Filed: June 7, 2001

Date: June 7, 2001

Title: NUCLEIC ACID SEQUENCES ENCODING TYPE III TENEBRIO
ANTIFREEZE PROTEINS AND METHOD FOR ASSAYING ACTIVITY

Assistant Commissioner for Patents
Washington, D.C. 20231

SUBMISSION OF "SEQUENCE LISTING"
AND COMPUTER READABLE COPY

Sir/Madame:

Submitted herewith are:

A. "Sequence Listings" for the nucleotide and/or amino acid sequences in this application, each "Sequence Listing" is assigned a separate identifier as required in 37 CFR Sections 1.821(c) and 37 CFR Sections 1.822 and 1.823;

B. A copy of each "Sequence Listing" submitted for this application in computer readable form in accordance with the requirements of 37 CFR Sections 1.821(e) and 1.824;

C. The following statement that the content of each "Sequence Listing" submitted and each computer readable copy are the same as required in 37 CFR Section 1.821(f).

I hereby state that the information recorded in computer readable form is identical to the written sequence listing.

0976340-0000

Respectfully submitted,

By: _____

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CERTIFICATE OF EXPRESS MAILING

10/20/50 0450 0450 0450

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Horwath, K. L. et al.
- (ii) TITLE OF INVENTION: Nucleic Acids Sequences Encoding Type III Tenebrio Antifreeze Proteins and Method for Assaying Activity.
- (iii) NUMBER OF SEQUENCES: 48
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSEE: Dr. Kathleen L. Horwath
 - (B) STREET: Department of Biological Sciences, Binghamton University
 - (C) CITY: Binghamton
 - (D) STATE: New York
 - (E) ZIP: 13902-6000
- (v) COMPUTER READABLE FORM
 - (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 - (B) COMPUTER: IBM AT/ATX compatible
 - (C) OPERATING SYSTEM: Windows 95/98
 - (D) SOFTWARE: Microsoft Word
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
 - (A) APPLICATION NUMBER: 60210446
 - (B) FILING DATE: June 8, 2000
- (viii) ATTORNEY/AGENT INFORMATION
 - (A) NAME: Mark Levy, Attorney-at-Law
 - (B) REGISTRATION NUMBER: 29,188
 - (C) REFERENCE/DOCKET NUMBER: RB125
- (ix) TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE: 607-722-6600
 - (B) TELEFAX: 607-724-2207

09676343-060704

```

(2) INFORMATION FOR SEQ. ID NO: 1
  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 19 Amino Acids
    (B) TYPE: Amino Acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: Peptide
  (iii) HYPOTHETICAL: no
  (iv) ANTI-SENSE: no
  (v) FRAGMENT TYPE: N-terminal fragment
  (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Tenebrio molitor
    (B) INDIVIDUAL/ISOLATE: none
    (C) CELL TYPE: fat body and whole organism
  (vii) IMMEDIATE SOURCE:
    (A) LIBRARY:
    (B) CLONE:
  (ix) FEATURES:
    (D) OTHER INFORMATION: N-terminal sequence of protein Tm 12.86
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```

```
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 Amino Acids  
    (B) TYPE: Amino Acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: Peptide  
(iii) HYPOTHETICAL: no  
(iv) ANTI-SENSE: no  
(v) FRAGMENT TYPE: N-terminal fragment  
(vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Tenebrio molitor  
    (B) INDIVIDUAL/ISOLATE: none  
    (C) CELL TYPE: fat body and whole organism  
(vii) IMMEDIATE SOURCE:  
    (A) LIBRARY:  
    (B) CLONE:  
(ix) FEATURES:  
    (D) OTHER INFORMATION: N-terminal sequence of protein Tm 12.86  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
```

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Non-his-tagged, signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

GTGGATCCAA AGAATTCGGC ACGAGACTAC TAAG ATG AAG TTG CTC      36
                               Met Lys Leu Leu
                               -15

TGT TGT CTA ATC TCC CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG      81
Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu
                               -10                               1
                               -5                               1

ACC GAG GCA CAA ATT GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT      126
Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys
                               5                               10                               15

CAA AAT GAA AGT GGA GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC      171
Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg
                               20                               25                               30

AAC GGT GAC TGG GAG GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT      216
Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe
                               35                               40                               45

TGC GTG GCC AGG AAC GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG      261
Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val
                               50                               55                               60

GTG GTC GAC GTG TTG AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC      306
Val Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn
                               65                               70                               75

GAC GAA GAA ACT GAG AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA      351
Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg
                               80                               85                               90

GAT ACT GTT GAA GAG ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG      396
Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met
                               95                               100                               105

AAA AAC AAG CCA AAG TTC TCA CCA GTT GAT TGA ACCACCACGA      439
Lys Asn Lys Pro Lys Phe Ser Pro Val Asp *
                               110                               115

CTAGTAGATG GTTCAAATGG TGTGCTTTAC ATATAAAAAAT AAAGTGTTC      489

TGATGTAAAA AAAAAAAAAA AAAAAAAAAA AACTCGAGAG TATTCTAGAG      539

CGGCCGCGGG CCCATCGTTT TCCACCC      566

```

(2) INFORMATION FOR SEQ. ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Tm 13.17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

Met Lys Leu Leu Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val
  -15                      -10                      -5

Gln Ala Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys
   1                      5                      10

Lys Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala
 15                      20                      25                      30

Arg Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe
 35                      40                      45

Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val
 50                      55                      60

Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu
 65                      70                      75

Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val
 80                      85                      90

Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro
 95                      100                      105                      110

Lys Phe Ser Pro Val Asp *
                      115

```

(2) INFORMATION FOR SEQ. ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for Tm 13.17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys
1          5          10          15
Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn
20          25          30
Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val
35          40          45
Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp
50          55          60
Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr
65          70          75          80
Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu
85          90          95
Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe
100         105         110
Ser Pro Val Asp *
115

```

(2) INFORMATION FOR SEQ. ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                -15                      -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA      91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                      1                      5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC      136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
    10                      15                      20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT      181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
    25                      30                      35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA      226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
    40                      45                      50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC      271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
    55                      60                      65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG      316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
    70                      75                      80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT      361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
    85                      90                      95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT      406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
   100                      105                      110

ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTAATA      455
Ile Asp *
   115

TCGTTATGTA AAAAAAAAAA AAAAAA      481

```


(2) INFORMATION FOR SEQ. ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.3

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                -15                      -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA      91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                      1                      5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC      136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
      10                      15                      20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT      181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                      30                      35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA      226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
      40                      45                      50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC      271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
      55                      60                      65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG      316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
      70                      75                      80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT      361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
      85                      90                      95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT      406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
      100                      105                      110

ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA      455
Ile Asp *
      115

TCGTTATGAA AAAAAAAAAA AAAAAAA      482

```

(2) INFORMATION FOR SEQ. ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2, 2.3, and 7.5

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Tm 12.84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
      -15                -10                -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
      1                5                10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
15                20                25                30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
      35                40                45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
      50                55                60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
      65                70                75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
      80                85                90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
95                100                105                110

Phe Ser Pro Ile Asp *
      115

```

(2) INFORMATION FOR SEQ. ID NO: 8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2, 2.3, and 7.5

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for T_m 12.84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
1          5          10          15
Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
20          25          30
Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
35          40          45
Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
50          55          60
Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp
65          70          75          80
Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
85          90          95
Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
100         105         110
Pro Ile Asp *
115

```

09076348-060704

(2) INFORMATION FOR SEQ. ID NO: 9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                -15                      -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA      91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                      1                      5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC      136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
      10                      15                      20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT      181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                      30                      35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA      226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
      40                      45                      50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC      271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
      55                      60                      65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG      316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
      70                      75                      80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT      361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
      85                      90                      95

GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT      406
Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
      100                      105                      110

ATT GAT TAA TTGTTTGTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA      455
Ile Asp *
      115

TCGTTATGTA AAAAAAAAAA AAAAAA      481

```

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino Acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: no

(vi) ORIGINAL SOURCE:

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(A) LIBRARY: cDNA

(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein for Clone 3.4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Phe Ser Pro Ile Asp *
115

(2) INFORMATION FOR SEQ. ID NO: 11

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein for Clone 3.4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
1          5          10          15

Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
20          25          30

Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
35          40          45

Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
50          55          60

Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp
65          70          75          80

Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
85          90          95

Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser
100         105         110

Pro Ile Asp *
115

```

(2) INFORMATION FOR SEQ. ID NO: 12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC      46
          Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                    -15                      -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA      91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
          -5                      1                      5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC      136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val Ser
          10                      15                      20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT      181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
          25                      30                      35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA      226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly
          40                      45                      50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC      271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
          55                      60                      65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG      316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
          70                      75                      80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT      361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
          85                      90                      95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT      406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
          100                      105                      110

ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA      455
Ile Asp *
          115

TCGTTATGAA AAAAAAAAAA AAAAAAA      482

```

(2) INFORMATION FOR SEQ. ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein for Clone 3.9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

Met Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
  -15                      -10                      -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
   1                      5                      10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
 35                      40                      45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu
 65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
 80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
 95                      100                      105                      110

Phe Ser Pro Ile Asp *
                  115

```

09076346-060704

(2) INFORMATION FOR SEQ. ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Mature protein for Clone 3.9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
1 5 10 15

Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
20 25 30

Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
35 40 45

Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
50 55 60

Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu Val Asp
65 70 75 80

Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
85 90 95

Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
100 105 110

Pro Ile Asp *

(2) INFORMATION FOR SEQ. ID NO: 15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(1) OTHER INFORMATION: Non-his-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                -15                      -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA      90
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                      1                      5

AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG TCC     136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
      10                      15                      20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT     181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                      30                      35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA     226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
      40                      45                      50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC     271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
      55                      60                      65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG     316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
      70                      75                      80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT     361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
      85                      90                      95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT     406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
      100                      105                      110

ATT GAT TAA TTGTTTTGTA TTTGGCTGAA TTTTGACAAT AAAGGTACTA      455
Ile Asp *
      115

TCGTTATGTA AAAAAAAAAA AAAAAA      481

```

- (2) INFORMATION FOR SEQ. ID NO: 16
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

F02090.04E02860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45 -40 -35	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	
-30 -25 -20	
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT	231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	
-15 -10 -5	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1 5 10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60 65 70	
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	
90 95 100	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105 110 115	
TTTGACTGAA TTTTGACAAT AAAGGTAATA TCGTTATGTA AAAAAAAAAA	645
AAAAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	681

(2) INFORMATION FOR SEQ. ID NO: 17

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
   -55                               -50                     -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
   -40                               -35                     -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
   -25                               -20                     -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
  -10                               -5                      1          5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
    10                               15                     20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
    25                               30                     35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
    40                               45                     50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
   55                               60                     65                     70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
    75                               80                     85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
    90                               95                     100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
   105                               110                     115

```

09676348-060704

- (2) INFORMATION FOR SEQ. ID NO: 18
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
- (ix) FEATURES
- (D) OTHER INFORMATION: His-tagged, signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

(2) INFORMATION FOR SEQ. ID NO: 19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
      -30                      -25                      -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
      -15                      -10                      -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
      1                      5                      10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
     15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
      35                      40                      45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
      50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
      65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
      80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
     95                      100                      105                      110

Phe Ser Pro Ile Asp *
                      115

```

(2) INFORMATION FOR SEQ. ID NO: 20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 682 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.3

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, Signal Plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA	CTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC		96
Met Gly Ser Ser His His His His His His Ser		
-55	-50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT		141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly		
-45	-40	-35
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG		186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met		
-30	-25	-20
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT		231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala		
-15	-10	-5
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC		276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser		
1	5	10
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC		321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp		
15	20	25
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG		366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys		
30	35	40
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC		411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala		
45	50	55
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG		456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val		
60	65	70
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC		501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val		
75	80	85
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT		546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys		
90	95	100
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGTA		595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *		
105	110	115
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA		645
AAAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT		682

T02099-04292960

(2) INFORMATION FOR SEQ. ID NO: 21

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.3

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
   -55                               -50                               -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
   -40                               -35                               -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
   -25                               -20                               -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
  -10                               -5                               1                               5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
   10                               15                               20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
   25                               30                               35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
   40                               45                               50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
   55                               60                               65                               70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
   75                               80                               85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
   90                               95                               100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
  105                               110                               115

```

0976348-060704

(i) SEQUENCE CHARACTERISTICS:

- | | | | | | |
|-----------------|-----------------|---------------------|---------------------|------------|-----|
| TTGTTAGCGG | ATGGAATTCC | CTCGTAGGGG | ATAATTTTGT | TTACTTTAAG | 50 |
| AAGGAGATAT | ACC | ATG GGC AGC AGC | CAT CAT CAT CAT CAT | CAC AGC | 96 |
| | Met Gly Ser Ser | His His His His His | | Ser | |
| | | -30 | | -25 | |
| AGC GGC CTG GTG | CCG CGC GGC AGC | CAT ATG GCT AGC | ATG ACT GGT | | 141 |
| Ser Gly Leu Val | Pro Arg Gly Ser | His Met Ala Ser | Met Thr Gly | | |
| | -20 | -15 | -10 | | |
| GGA CAG CAA ATG | GGT CGC GGA TCC | CTC ACC GAC GAA | CAG ATA CAG | | 186 |
| Gly Gln Gln Met | Gly Arg Gly Ser | Leu Thr Asp Glu | Gln Ile Gln | | |
| | -5 | 1 | 5 | | |
| AAA AGG AAC AAG | ATC AGC AAA GAA | TGC CAG CAG GTG | TCC GGA GTG | | 231 |
| Lys Arg Asn Lys | Ile Ser Lys Glu | Cys Gln Gln Val | Ser Gly Val | | |
| | 10 | 15 | 20 | | |
| TCC CAA GAG ACG | ATC GAC AAA GTC | CGC ACA GGT GTC | TTG GTC GAT | | 276 |
| Ser Gln Glu Thr | Ile Asp Lys Val | Arg Thr Gly Val | Leu Val Asp | | |
| | 25 | 30 | 35 | | |
| GAT CCC AAA ATG | AAG AAG CAC GTC | CTC TGC TTC TCG | AAG AAA ACT | | 321 |
| Asp Pro Lys Met | Lys Lys His Val | Leu Cys Phe Ser | Lys Lys Thr | | |
| | 40 | 45 | 50 | | |
| GGA GTG GCA ACC | GAA GCC GGA GAC | ACC AAT GTG GAG | GTA CTC AAA | | 366 |
| Gly Val Ala Thr | Glu Ala Gly Asp | Thr Asn Val Glu | Val Leu Lys | | |
| | 55 | 60 | 65 | | |
| GCC AAG CTG AAG | CAT GTG GCC AGC | GAC GAA GAA GTG | GAC AAG ATC | | 411 |
| Ala Lys Leu Lys | His Val Ala Ser | Asp Glu Glu Val | Asp Lys Ile | | |
| | 70 | 75 | 80 | | |
| GTG CAG AAG TGC | GTG GTC AAG AAG | GCC ACA CCA GAG | GAA ACG GCT | | 456 |
| Val Gln Lys Cys | Val Val Lys Lys | Ala Thr Pro Glu | Glu Thr Ala | | |
| | 85 | 90 | 95 | | |
| TAT GAC ACC TTC | AAG TGT ATT TAC | GAC AGT AAA CCT | GAT TTC TCT | | 501 |
| Tyr Asp Thr Phe | Lys Cys Ile Tyr | Asp Ser Lys Pro | Asp Phe Ser | | |
| | 100 | 105 | 110 | | |
| CCT ATT GAT TAA | CTCGAGCACC | ACCACCACCA | CCACTGAGAT | | 543 |
| Pro Ile Asp * | | | | | |
| | 115 | | | | |

(2) INFORMATION FOR SEQ. ID NO: 23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.3

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
      -30                      -25                      -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
      -15                      -10                      -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
      1                      5                      10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
     15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
      35                      40                      45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
      50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
      65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
      80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
      95                      100                      105                      110

Phe Ser Pro Ile Asp *
                      115

```

- (2) INFORMATION FOR SEQ. ID NO: 24
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

09076340-000001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-65 -60 -55	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-50 -45 -40	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile	
-35 -30 -25	
CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC	231
Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser	
-20 -15 -10	
CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT	276
Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile	
-5 1 5	
GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA	321
Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly	
10 15 20	
GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG	366
Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu	
25 30 35	
GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC	411
Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn	
40 45 50	
GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG	456
Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu	
55 60 65	
AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG	501
Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu	
70 75 80	
AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG	546
Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu	
85 90 95	
ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG	595
Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys	
100 105 110	
TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG	643
Phe Ser Pro Val Asp *	
115	
TGTGCTTTAC ATATAAAAT AAAGTGTTTC TGATGTAAAA AAAAAAAAAA	693
AAAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT	743
TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT	777

(2) INFORMATION FOR SEQ. ID NO: 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
  -55                      -50                      -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
  -40                      -35                      -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Cys Leu Ile
  -25                      -20                      -15                      -10

Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile
           -5                      1                      5

Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val
           10                      15                      20

Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp
           25                      30                      35

Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly Leu
           40                      45                      50

Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu Lys Val
           55                      60                      65                      70

Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys
           75                      80                      85

Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe
           90                      95                      100

Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser Pro Val Asp *
           105                      110                      115

```


(2) INFORMATION FOR SEQ. ID NO: 27

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
      -30                      -25                      -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
      -15                      -10                      -5

Gly Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys
  1                      5                      10                      15

Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg
      20                      25                      30

Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys
      35                      40                      45

Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val
      50                      55                      60

Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu
      65                      70                      75

Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu
      80                      85                      90                      95

Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys
      100                      105                      110

Phe Ser Pro Val Asp *
      115

```

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: no

(vi) ORIGINAL SOURCE

(B) INDIVIDUAL/ISOLATE: none

IMMEDIATE SOURCE:

(B) CLONE: 3.4

FEATURES

(D) OTHER INFORMATION: His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45 -40 -35	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	
-30 -25 -20	
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT	231
Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	
-15 -10 -5	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1 5 10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60 65 70	
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG GTT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Val	
90 95 100	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGTA	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105 110 115	
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGTA AAAAAAAAAA	645
AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	681

09075349 "DEP" 04

(2) INFORMATION FOR SEQ. ID NO: 29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
   -55                               -50                       -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
   -40                               -35                       -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
   -25                               -20                       -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
  -10                               -5                        1      5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
    10                               15                       20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
    25                               30                       35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
    40                               45                       50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
   55                               60                       65      70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
    75                               80                       85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
    90                               95                       100

Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
   105                               110                       115

```

096746-0074

- (2) INFORMATION FOR SEQ. ID NO: 30
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v)
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
- (ix) FEATURES
- (D) OTHER INFORMATION: His-tagged, Signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CCT ATT GAT TAA CTCGAGCAC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

(2) INFORMATION FOR SEQ. ID NO: 31

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
 1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp
95 100 105 110

Phe Ser Pro Ile Asp *
115

- (2) INFORMATION FOR SEQ. ID NO: 32
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

09475349-060704
T04090-0402050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA	50
AGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45 -40 -35	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	
-30 -25 -20	
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT	231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	
-15 -10 -5	
CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1 5 10	
AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp	
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala	
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60 65 70	
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	
90 95 100	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGT	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105 110 115	
TTTGA	645
TTTGA	682

(2) INFORMATION FOR SEQ. ID NO: 33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.9

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
   -55                               -50                               -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
   -40                               -35                               -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
   -25                               -20                               -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
  -10                               -5                               1                               5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val
   10                               15                               20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
   25                               30                               35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly Val
   40                               45                               50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
   55                               60                               65                               70

Lys HisVal Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
   75                               80                               85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
   90                               95                               100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
  105                               110                               115

```


(2) INFORMATION FOR SEQ. ID NO: 35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.9

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
      -30                      -25                      -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
      -15                      -10                      -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
      1                      5                      10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
     15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
      35                      40                      45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
      50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
      65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
      80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
      95                      100                      105                      110

Phe Ser Pro Ile Asp *
      115

```

RB125 RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45 -40 -35	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	
-30 -25 -20	
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT	231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	
-15 -10 -5	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1 5 10	
AAA GAG TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60 65 70	
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	
90 95 100	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105 110 115	
TTTGGCTGAA TTTTGACAAT AAAGGTACTA TCGTTATGTA AAAAAAAAAA	645
AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	681

(2) INFORMATION FOR SEQ. ID NO: 37

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 7.5

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
   -55                               -50                       -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
   -40                               -35                       -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
   -25                               -20                       -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
  -10                               -5                        1      5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
   10                               15                       20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
   25                               30                       35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
   40                               45                       50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
   55                               60                       65      70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
   75                               80                       85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
   90                               95                       100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
  105                               110                       115

```

(2) INFORMATION FOR SEQ. ID NO: 38

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, Signal minus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

(2) INFORMATION FOR SEQ. ID NO: 39

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 7.5

(ix) FEATURES

- (D) OTHER INFORMATION: Mature protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

```

Met Gly Ser Ser His His His His Ser Ser Gly Leu Val Pro
   -30                      -25                      -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
   -15                      -10                      -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
    1                      5                      10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
  15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
   35                      40                      45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
   50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
   65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
   80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
   95                      100                      105                      110

Phe Ser Pro Ile Asp *
                   115

```

09076348-000704

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: no

(vi) ORIGINAL SOURCE:

(B) INDIVIDUAL/ISOLATE: none

(vii) IMMEDIATE SOURCE:

(B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5

(D) OTHER INFORMATION: Tm 12.84 upper primer with Bam-HI site

CGCGGATCCC TCACCGACGA ACAG

RB125 RT

- (2) INFORMATION FOR SEQ. ID NO: 41
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Tm 12.84 lower primer with XhoI site
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAGAGGATAA CTAATTGAGC TCGCC 25

03076349-060704

- (2) INFORMATION FOR SEQ. ID NO: 42
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v)
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Tm 13.17 upper primer with Bam-HI site
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CGCGGATCCC TGACCGAGGC ACAA 24

(2) INFORMATION FOR SEQ. ID NO: 43

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Tm 13.17 lower primer with XhoI site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GAGTGGTCAA CTAAGTGGC TCGCC 25

T02090-04292050

(2) INFORMATION FOR SEQ. ID NO: 44

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

- (D) OTHER INFORMATION: Consensus of the Tm 12.84 Isoforms

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCN TTC GCC GCC      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                -15                      -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAY GAA CAG ATA CAG AAA      91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                      1                      5

AGG AAC AAG ATC AGC AAA GAR TGC CAG CAG GNG TCC GGA GTG TCC      136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
    10                      15                      20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAY GAT      181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
    25                      30                      35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG ARA ACT GGA      226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
    40                      45                      50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC      271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
    55                      60                      65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAR GTG GAC AAG ATC GTG      316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
    70                      75                      80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT      361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
    85                      90                      95

GAC ACC TTC AAG NNT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT      406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
   100                      105                      110

ATT GAT TAA TTGTTTGTGTA TTTGRCTGAA TTTTGACAAT AAAGGTANTA      455
Ile Asp *
   115

TCGTTATGNA AAAAAAAAAA AAAAAA      481

```

(2) INFORMATION FOR SEQ. ID NO: 45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

- (D) OTHER INFORMATION: Consensus of Seq ID #44 with Tm 13.17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

GGCANRNNNN AAR ATG AAR YTN CTC TNN TGY YTN RYN TYC NYC RYY      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                        -15                        -10

NTN NTN RTC RNA GYT CAG GCY CTN ACC GAN GNA CAR ATN NAG AAA      91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                        1                        5

NNG AAC AAG ATC AGC AAA RAR TGY CAR NAN GNR NNY GGA GTG TCN     136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
      10                        15                        20

CAA GAG AYN ATN RNC AAA GYY CGC ANN GGT GNC TNG GNN GAY GAT     181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                        30                        35

CCY AAA NTG AAR NRN CAN GTY YTY TGC NTN NCN ARG ARN RCY GGN     226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
      40                        45                        50

NTG GCN ACN GAA NCN GGA GAN RYN RNN GTN GAN GTR YTN ARR GNN     271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
      55                        60                        65

AAG NTG ARG NAN GTN RCY RRC AAC GAC GAA GAR RYN GAN AAR ATC     316
Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile
      70                        75                        80

RTN NAN AAG TGC GYN GTC AAG ARR GNY ACN NYN GAR GAR ACG GYN     361
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala
      85                        90                        95

TNY RAY ACY TTC AAR NNT RTY NNN RAN ARY AAR CCN RAN TTC TCN     406
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
      100                        105                        110

CCN RTT GAT TRA NYNNYYNNNA YTNNGNNNRNR NTTYRANAAT AAAGNNNNTN     458
Pro Ile Asp *
      115

TNRTNNNRNA AAAAAAAAAA AAAAAA      484

```

(2) INFORMATION FOR SEQ. ID NO: 46

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Consensus of Seq ID #45 with B1/B2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

GGCANRNNNN AAR ATG AAR YTN CTC TNN TGY YTN RYN TYY NYC RYY      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                -15                      -10

NTN NTN RTC NNA GYT CAG GCY NTN ACY NAN GNA NAN NTN NAG NNA      91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                      1                      5

NNG NNC NAR AYC AGC RNA RAR TGY NAR NNN GNR NNY GGA GTG TCN      136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
      10                      15                      20

NAA GAN RYN ATN RNN ARA GYY CGC ANN GGT GNC TNG GNN GAY GAY      181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                      30                      35

CCY AAA NTG AAR NNN CAN NTY YTY TGC NTN NYN ARG RNN NYY GRN      226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
      40                      45                      50

NTR GYN RCN GAA NCN GGA GAN RYN RNN GYN GAN RYR YTN ARR GNN      271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
      55                      60                      65

AAG NTG ANG NRN NNN NNN RNN ANN RNN RAR RAR RYN RRN ARR NTN      316
Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile
      70                      75                      80

NYN NRN ARN NNN NNN NNN NNG ARN RNN NYN NNN RAR RNR NNN NNN      361
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala
      85                      90                      95

TNN RAN NYN YYN AAN NNN NNY NNN RRN ANN ARN CCN RNN TYY TYN      406
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
      100                      105                      110

CNN RYT RNT TRN NYNNNNNNNN YNNGNNNRNR NTTYRANAAT AAAGNNNYTN      458
Pro Ile Asp *
      115

TNRTNNNRNA AAAAAAAAAA AAAAAA      484

```

- (2) INFORMATION FOR SEQ. ID NO: 47
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Consensus of Seq. ID #46 with AFP-3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGC	NNR	NNNN	AAR	ATG	AAR	YTN	CTC	YNN	TGY	YTN	RYN	YYY	NYY	RYY	46
					Met	Lys	Leu	Leu	Leu	Cys	Phe	Ala	Phe	Ala	Ala
							-15							-10	
NTN	NTN	RYC	NNR	RYY	YAN	GCY	NTN	ACY	NAN	RNA	NNN	NNN	NAG	NNR	91
Ile	Val	Ile	Gly	Ala	Gln	Ala	Leu	Thr	Asp	Glu	Gln	Ile	Gln	Lys	
		-5					1				5				
NNG	NNY	NAR	NNC	AGC	RNN	RNN	TGY	NAR	NNN	GNR	NNY	GGA	GTR	TCN	136
Arg	Asn	Lys	Ile	Ser	Lys	Glu	Cys	Gln	Gln	Glu	Ser	Gly	Val	Ser	
	10					15					20				
NAA	GAN	NYN	NTN	RNN	ARR	GYY	CGC	ANN	NGT	GNN	NNR	GNN	GAY	GAY	181
Gln	Glu	Thr	Ile	Asp	Lys	Val	Arg	Thr	Gly	Val	Leu	Val	Asp	Asp	
	25					30					35				
CCY	AAA	NTG	AAR	NNN	CAN	NYN	YTY	TGC	NTN	NYN	ARG	RNN	NYN	GRN	226
Pro	Lys	Met	Lys	Lys	His	Val	Leu	Cys	Phe	Ser	Lys	Lys	Thr	Gly	
	40					45					50				
NTN	RYN	RNN	GNN	NNN	GGN	GAN	NYN	NNN	NYN	GAN	NNN	NTN	ARR	RNN	271
Val	Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn	Val	Glu	Val	Leu	Lys	Ala	
	55					60					65				
AAR	NTN	ANG	NRN	NNN	NNN	RNN	RNN	NNN	RAR	RAR	RYN	RRN	RRN	NTN	316
Lys	Leu	Lys	His	Val	Ala	Ser	Asn	Asp	Glu	Glu	Val	Asp	Lys	Ile	
	70					75					80				
NYN	NNN	ARN	NNN	NNN	NNN	NNG	ARN	RNN	NYN	NNN	NAR	NNN	NNN	NNN	361
Val	Gln	Lys	Cys	Val	Val	Lys	Lys	Ala	Thr	Pro	Glu	Glu	Thr	Ala	
	85					90					95				
NNN	RAN	NYN	YYN	AAN	NNN	NNY	NNN	RRN	ANN	ARN	YCN	NNN	TNN	NNN	406
Tyr	Asp	Thr	Phe	Lys	Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp	Phe	Ser	
	100					105					110				
CNN	NYN	RNN	TRN	NNNNNNNNNN	YNNRNNNNNN	NNNNNNNAAT	AAANNNNNNN								458
Pro	Ile	Asp	*												
	115														
NNNNNNNNNA	AAAAAAAAAA	AAAAAA													484

- (2) INFORMATION FOR SEQ. ID NO: 48
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE:
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Genral Consensus of Clones,
B1, B2 and AFP-3

10/20/90 04:29:40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
      Cys      Leu Ile Ser Leu Ile Leu Leu Val Thr Val
              Thr Leu Val
              Val
      -15          -10          -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
Tyr      Ile      Glu Ala Asp Leu Glu Leu Leu Arg Arg Gln Thr  Ala
      1          5          10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
Lys      Lys Asn Val      Ala      Glu Asp Ile Leu Thr Arg Ala
Ala      Thr Ala
      15          20          25          30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
      Asn Arg Asp Trp Glu      Leu      Arg Gln Leu Phe
      Lys      Glu Glu
              35          40          45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
      Val Ala Arg Arg Ala Ile Leu Val Ala Ser      Glu Ile Glu
      Ile Phe      Ala Leu Glu Ile Ile Asp      Val Val
      Leu      Asn      Glu Phe      Phe Gln
              50          55          60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser *** Asp Glu
Ala Asp Thr Phe Arg Glu      Val Thr Arg Asn Thr Asn Asp Pro
Leu      His Ile      Thr      Phe Arg Lys      Ser Asp Asn
              65          70          75

Glu Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro
Lys Ser Glu Asp Leu Ile Glu      Asn      Thr      Glu Asp  Val
      Thr
      80          85          90

Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro
Gln Asp Ser Val Phe Glu Val Thr      Val Val Leu Lys Asn Arg Ser
      His      Ser Ala Asn Phe
              95          100          105          110

Asp Phe Ser Pro Ile Asp *** *** *
Asn      Phe Gly Asp Leu Phe Val *
Lys
      115

```

09676348-060704
 T0900-0904